

RAW SEQUENCE LISTING **ERROR REPORT**

CRFI to be filed
BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/065,200
Source: OIPE
Date Processed by STIC: 9-26-02

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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
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<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
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Revised 01/29/2002

Does Not Comply
Corrected Diskette Needed
See page 7



OIEP

RAW SEQUENCE LISTING

DATE: 09/26/2002

PATENT APPLICATION: US/10/065,200

TIME: 07:37:29

Input Set : N:\Crif3\Datahold\EFS\10065200\FC-4-1.txt

Output Set: N:\CRF4\09262002\J065200.raw

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3 <110> APPLICANT: Wisnewski, Nancy
4   Becher, Anna M.
5   Jarvis, Eric
7 <120> TITLE OF INVENTION: NOVEL FLEA ECDYSONE AND ULTRASPIRACLE NUCLEIC ACID
8   MOLECULES, PROTEINS AND USES THEREOF
10 <130> FILE REFERENCE: FC-4-1
C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/065,200
13 <141> CURRENT FILING DATE: 2002-09-25
15 <150> PRIOR APPLICATION NUMBER: 09/435,019
16 <151> PRIOR FILING DATE: 1999-11-05
18 <150> PRIOR APPLICATION NUMBER: 60/107,559
19 <151> PRIOR FILING DATE: 1998-11-06
21 <160> NUMBER OF SEQ ID NOS: 71
23 <170> SOFTWARE: PatentIn Ver. 2.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 446
27 <212> TYPE: DNA
28 <213> ORGANISM: Ctenocephalides felis
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35 aaatctgctg ctcccttagc gaattctgca ttacttcaga agcctgatat ttgacctgcg 180
37 gtcataaagt ggcacccatt acctccagaa gcaactaaag tgaaattttt gtcagacaag 240
39 attcttgctg aaaacagaat tcgaaatgtt ccacctttga ctgcaaatca agaatatgtg 300
41 atcgcaagat tagtggtgta ccaagatgga tatgaacaac cttctgagga agacctacga 360
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50 <212> TYPE: DNA
51 <213> ORGANISM: Ctenocephalides felis
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58 tcttggtacc aactaatct tgcgacaca tattcttgat ttgcagtcaa aggtggaaca 180
60 tttcgaaatt tgttttcagc agaatacttg tctgacaaaa atttcacttt agttgcttct 240
62 ggaggtaatg ggtgcattt catgaccgca ggcaaaatat caggcttctg aagtaatgca 300
64 gaattcgcta agggagcagc agattttcca acggtacctg atattggtcc gatgtccttt 360
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68 tcggggcgca ttccgacagc caaaca 446
71 <210> SEQ ID NO: 3
72 <211> LENGTH: 350
73 <212> TYPE: DNA

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Input Set : N:\Crif3\Datahold\EFS\10065200\FC-4-1.txt

Output Set: N:\CRF4\09262002\J065200.raw

74 <213> ORGANISM: Ctenocephalides felis

76 <400> SEQUENCE: 3

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81 cggtcagtga atgcgacca ttacctccag aagcaactaa agtgaaaattt ttgtcagaca 180
83 agattcttgc tgaaaacaga attcgaaatg ttccaccttt gactgcaaat caagaatatg 240
85 tgatcgcaag attagtgtgg taccaagatg gatatgaaca accttctgag gaagacctac 300
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92 <212> TYPE: DNA

93 <213> ORGANISM: Ctenocephalides felis

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100 atttgcagtc aaagggtggaa catttcgaat tctgttttca gcaagaatct tgtctgacaa 180
102 aaatttcaact ttagttgctt ctggaggtaa tgggtcgcat ttcatgaccg caggcaaaat 240
104 atcaggcttc tgaaggaaatg cagaattcgc taaggaggca gcagattttc caacggtacc 300
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111 <212> TYPE: DNA

112 <213> ORGANISM: Ctenocephalides felis

114 <220> FEATURE:

115 <221> NAME/KEY: CDS

116 <222> LOCATION: (605)..(2287)

118 <400> SEQUENCE: 5

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123 tctatcaatc agaaatgata attaaacaat ttttttatat tgaaatagaa catattatgt 180
125 tcatatgtca ataacaaatt ttaaaccattc atccaagtta cctattttat gcttttaaga 240
127 tattatttat ttatttatatt tgttttgtaa aattttaaat ttacataaaa tactttctaa 300
129 ctatgaatat aaattaatat acaaaagatt ttgaaactaa gaggaaaagt aattataatc 360
131 attttaatca ttaaattata tactcaaaat gatacaatta gattttacag tcacacacat 420
133 taggtacaga gattcaatta tgaattagga gttgagaaat gctttcgagt aaaatctgca 480
135 ataagatgac tatattccta aggatgttat gtcagtcata aataaaaaatc actatatttt 540
137 caatttgtgt atgggtgatct tctaaaggat aaatgtgtga agtgaaatac cttgcattat 600
139 caac atg aaa cga cgt tgg tct aac aac ggt ggc ttc caa acc ttg cgg 649
140 Met Lys Arg Arg Trp Ser Asn Asn Gly Gly Phe Gln Thr Leu Arg
141 1 5 10 15
143 atg ctc gaa gat gtt gca tct ggt gag gta acg tcg tct tct ggt ggc 697
144 Met Leu Glu Asp Val Ala Ser Gly Glu Val Thr Ser Ser Ser Gly Gly
145 20 25 30
147 gcc ctg gct gcg ttg agt ccg gct tcg tta ggt tcg ccc gag aca tat 745
148 Ala Leu Ala Ala Leu Ser Pro Ala Ser Leu Gly Ser Pro Glu Thr Tyr
149 35 40 45
151 gcc gag ctg gat ttg tgg gtg tac gag gaa gct ggc tta cat cca ggt 793
152 Ala Glu Leu Asp Leu Trp Val Tyr Glu Glu Ala Gly Leu His Pro Gly
153 50 55 60

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Input Set : N:\Crif3\Datahold\EFS\10065200\FC-4-1.txt

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155 tca ggt gtg caa gga tgc ggt gcg gtc gcc gcc ttg cca tcg atc gcg 841
156 Ser Gly Val Gln Gly Cys Gly Ala Val Ala Ala Leu Pro Ser Ile Ala
157      65              70              75
159 aca cag gtc ccc cta gga ttg ccc gct atg gac cta ccg cac acg cct 889
160 Thr Gln Val Pro Leu Gly Leu Pro Ala Met Asp Leu Pro His Thr Pro
161 80      85      90      95
163 cgg agt gac agt gcg ggt agc atc tca tca gga cga gaa gac ctg tca 937
164 Arg Ser Asp Ser Ala Gly Ser Ile Ser Ser Gly Arg Glu Asp Leu Ser
165      100      105      110
167 ccg cct agt tct ttg aac ggc tat tca gca gat ggc tgc gaa gcg aag 985
168 Pro Pro Ser Ser Leu Asn Gly Tyr Ser Ala Asp Gly Cys Glu Ala Lys
169      115      120      125
171 aag gcc aag aaa ggg ccg gcg ccg cgg cag cag gag gaa cta tgt ctt 1033
172 Lys Ala Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu Glu Leu Cys Leu
173      130      135      140
175 gtg tgc ggc gac cgt gcc tcc gga tat cat tac aac gct ctt act tgt 1081
176 Val Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys
177      145      150      155
179 gaa gga tgc aaa ggt ttt ttc cga cga agt gtg act aag aat gcc gtg 1129
180 Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn Ala Val
181 160      165      170      175
183 tac gtg tgc aag ttt ggg cac acg tgc gaa atg gac atg tat atg cga 1177
184 Tyr Val Cys Lys Phe Gly His Thr Cys Glu Met Asp Met Tyr Met Arg
185      180      185      190
187 cgc aaa tgt cag gaa tgt agg ctc aag aaa tgt ttg gct gtc gga atg 1225
188 Arg Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met
189      195      200      205
191 cgc ccc gag tgc gtg gtt ccc gaa aac caa tgc gcc atg aag cga aag 1273
192 Arg Pro Glu Cys Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Lys
193      210      215      220
195 gaa aag aag gca cag aag gaa aag gac atc gga cca ata tca ggt acc 1321
196 Glu Lys Lys Ala Gln Lys Glu Lys Asp Ile Gly Pro Ile Ser Gly Thr
197      225      230      235
199 gtt gga aaa tct gct gct ccc tta gcg aat tct gca tta ctt cag aag 1369
200 Val Gly Lys Ser Ala Ala Pro Leu Ala Asn Ser Ala Leu Leu Gln Lys
201 240      245      250      255
203 cct gat att ttg cct gcg gtc atg aaa tgc gac cca tta cct cca gaa 1417
204 Pro Asp Ile Leu Pro Ala Val Met Lys Cys Asp Pro Leu Pro Pro Glu
205      260      265      270
207 gca act aaa gtg aaa ttt ttg tca gac aag att ctt gct gaa aac aga 1465
208 Ala Thr Lys Val Lys Phe Leu Ser Asp Lys Ile Leu Ala Glu Asn Arg
209      275      280      285
211 att cga aat gtt cca cct ttg act gca aat caa gaa tat gtg atc gca 1513
212 Ile Arg Asn Val Pro Pro Leu Thr Ala Asn Gln Glu Tyr Val Ile Ala
213      290      295      300
215 aga tta gtg tgg tac caa gat gga tat gaa caa cct tct gag gaa gac 1561
216 Arg Leu Val Trp Tyr Gln Asp Gly Tyr Glu Gln Pro Ser Glu Glu Asp
217      305      310      315
219 cta cga agg ata atg ata agt aca cca gct gaa gat gaa gct ctt gaa 1609

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223 ttt cgg cat ata act gaa att acc ata ctt act gtg cag ctt ata gtg 1657
224 Phe Arg His Ile Thr Glu Ile Thr Ile Leu Thr Val Gln Leu Ile Val
225          340          345          350
227 gaa ttt gca aag ggt tta cca gct ttt acc aaa ata cca caa gaa gat 1705
228 Glu Phe Ala Lys Gly Leu Pro Ala Phe Thr Lys Ile Pro Gln Glu Asp
229          355          360          365
231 caa ata aca tta tta aag gca tgt tca agt gaa gta atg atg ctg cga 1753
232 Gln Ile Thr Leu Leu Lys Ala Cys Ser Ser Glu Val Met Met Leu Arg
233          370          375          380
235 atg gct cgg cgg tac gat gca gtg tcg gat tca atc tta ttc gcg aat 1801
236 Met Ala Arg Arg Tyr Asp Ala Val Ser Asp Ser Ile Leu Phe Ala Asn
237          385          390          395
239 aat cgt tca tat act cgt gac tcc tat aaa atg gct ggt atg gca gat 1849
240 Asn Arg Ser Tyr Thr Arg Asp Ser Tyr Lys Met Ala Gly Met Ala Asp
241 400          405          410          415
243 aca ata gaa gat cta ttg cat ttt tgt cga cag atg tat act atg act 1897
244 Thr Ile Glu Asp Leu Leu His Phe Cys Arg Gln Met Tyr Thr Met Thr
245          420          425          430
247 gta gac aat gtg gag tat gca cta ata aca gca att gtg att ttt tca 1945
248 Val Asp Asn Val Glu Tyr Ala Leu Ile Thr Ala Ile Val Ile Phe Ser
249          435          440          445
251 gat cga cct gga ttg gaa caa gca gat ctt gtg gaa caa att caa agt 1993
252 Asp Arg Pro Gly Leu Glu Gln Ala Asp Leu Val Glu Gln Ile Gln Ser
253          450          455          460
255 tat tac atc aaa aca tta aag tgc tac att ttg aat cga cat agt ggt 2041
256 Tyr Tyr Ile Lys Thr Leu Lys Cys Tyr Ile Leu Asn Arg His Ser Gly
257          465          470          475
259 gac cct aag tgt gga ata ttg ttt gcc aaa ctt ctt tct att ctt act 2089
260 Asp Pro Lys Cys Gly Ile Leu Phe Ala Lys Leu Leu Ser Ile Leu Thr
261 480          485          490          495
263 gaa tta cgc acg tta gga aat caa aac tca gaa atg tgt ttt gca ctg 2137
264 Glu Leu Arg Thr Leu Gly Asn Gln Asn Ser Glu Met Cys Phe Ala Leu
265          500          505          510
267 aaa ttg aag aac aga aaa ctt cct aga ttt tta gaa gaa att tgg gat 2185
268 Lys Leu Lys Asn Arg Lys Leu Pro Arg Phe Leu Glu Glu Ile Trp Asp
269          515          520          525
271 gtg aca gat aat gtg cct cct acg ata gac agc atg cat agt gta tcg 2233
272 Val Thr Asp Asn Val Pro Pro Thr Ile Asp Ser Met His Ser Val Ser
273          530          535          540
275 gag aat ttc tat aat aat gaa agt aat ggt acc agt gat tct aca cca 2281
276 Glu Asn Phe Tyr Asn Asn Glu Ser Asn Gly Thr Ser Asp Ser Thr Pro
277          545          550          555
279 atg taa agtgctcaga aaatcaacag ctcttttgca tatttggtta ctgtgtactg 2337
280 Met
281 560
283 gtatggaaaa ttaaggtaac attaaaaatat tacataagca ccatgggaaa aggccgttaa 2397
285 ggcaatatatt ttgaataaat aatctattga gacggtacca atggtaaact tggaaaaaat 2457

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Output Set: N:\CRF4\09262002\J065200.raw

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287 tcttctgttt acatattagg agccaagtta aagaataagt atgaatgatt gttgataaat 2517
289 tgcttgtgta acacttcaat ggccttcaat aaaataatgt ttaacaacgt cgataggaaa 2577
291 ttaaaaagaa atcatgtgta ataaaatcat ttgtaggccg gccatactga tttacctata 2637
293 ttaagcagaa acttcttaat gtataaatat atttttgctt tgcaaggtaa aaccttctca 2697
295 atgcaacaat gaattatata tataaacatt gattatttta tcgttagaat ttgaattttg 2757
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303 <211> LENGTH: 560
304 <212> TYPE: PRT
305 <213> ORGANISM: Ctenocephalides felis
307 <400> SEQUENCE: 6
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311 Leu Glu Asp Val Ala Ser Gly Glu Val Thr Ser Ser Ser Gly Gly Ala
312 20 25 30
314 Leu Ala Ala Leu Ser Pro Ala Ser Leu Gly Ser Pro Glu Thr Tyr Ala
315 35 40 45
317 Glu Leu Asp Leu Trp Val Tyr Glu Glu Ala Gly Leu His Pro Gly Ser
318 50 55 60
320 Gly Val Gln Gly Cys Gly Ala Val Ala Ala Leu Pro Ser Ile Ala Thr
321 65 70 75 80
323 Gln Val Pro Leu Gly Leu Pro Ala Met Asp Leu Pro His Thr Pro Arg
324 85 90 95
326 Ser Asp Ser Ala Gly Ser Ile Ser Ser Gly Arg Glu Asp Leu Ser Pro
327 100 105 110
329 Pro Ser Ser Leu Asn Gly Tyr Ser Ala Asp Gly Cys Glu Ala Lys Lys
330 115 120 125
332 Ala Lys Lys Gly Pro Ala Pro Arg Gln Gln Glu Glu Leu Cys Leu Val
333 130 135 140
335 Cys Gly Asp Arg Ala Ser Gly Tyr His Tyr Asn Ala Leu Thr Cys Glu
336 145 150 155 160
338 Gly Cys Lys Gly Phe Phe Arg Arg Ser Val Thr Lys Asn Ala Val Tyr
339 165 170 175
341 Val Cys Lys Phe Gly His Thr Cys Glu Met Asp Met Tyr Met Arg Arg
342 180 185 190
344 Lys Cys Gln Glu Cys Arg Leu Lys Lys Cys Leu Ala Val Gly Met Arg
345 195 200 205
347 Pro Glu Cys Val Val Pro Glu Asn Gln Cys Ala Met Lys Arg Lys Glu
348 210 215 220
350 Lys Lys Ala Gln Lys Glu Lys Asp Ile Gly Pro Ile Ser Gly Thr Val
351 225 230 235 240
353 Gly Lys Ser Ala Ala Pro Leu Ala Asn Ser Ala Leu Leu Gln Lys Pro
354 245 250 255
356 Asp Ile Leu Pro Ala Val Met Lys Cys Asp Pro Leu Pro Pro Glu Ala
357 260 265 270
359 Thr Lys Val Lys Phe Leu Ser Asp Lys Ile Leu Ala Glu Asn Arg Ile
360 275 280 285
362 Arg Asn Val Pro Pro Leu Thr Ala Asn Gln Glu Tyr Val Ile Ala Arg

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 09/26/2002
PATENT APPLICATION: US/10/065,200 TIME: 07:37:30

Input Set : N:\Crf3\Datahold\EFS\10065200\FC-4-1.txt
Output Set: N:\CRF4\09262002\J065200.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:45; N Pos. 15

Seq#:51; N Pos. 10

VARIABLE LOCATION SUMMARY

DATE: 09/26/2002

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Input Set : N:\Crif3\Datahold\EFS\10065200\FC-4-1.txt

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Use of n's or Xaa's(NEW RULES):

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of <220> to <223> is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:45; N Pos. 15

Seq#:51; N Pos. 10

VERIFICATION SUMMARY

DATE: 09/26/2002

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Input Set : N:\Crif3\Datahold\EFS\10065200\FC-4-1.txt

Output Set: N:\CRF4\09262002\J065200.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2775 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:32
L:3458 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:45
L:3458 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:45
L:3458 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:45 after pos.:0
L:3536 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:51
L:3536 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:51
L:3536 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:51 after pos.:0